

O/PK

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/236,995B

CRF Processing Date: 8/14/2001
Edited by: Ar
Verified by: Ar (STIC sig)

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TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filenam at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/236,995B

DATE: 08/14/2001
 TIME: 15:54:41

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\08142001\I236995B.raw

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3 <110> APPLICANT: Mahajan, Pramod B.
 4 Zuo, Zhuang
 6 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and Its Uses
 8 <130> FILE REFERENCE: 5718-34, 035718-174234
 10 <140> CURRENT APPLICATION NUMBER: 09/236,995B
 11 <141> CURRENT FILING DATE: 1999-01-26
 13 <150> PRIOR APPLICATION NUMBER: 60/072,785
 14 <151> PRIOR FILING DATE: 1998-01-27
 16 <160> NUMBER OF SEQ ID NOS: 5
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2949
 22 <212> TYPE: DNA
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 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(2949)
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 30 <221> NAME/KEY: misc_feature
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 41 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
 42 1 5 10 15
 44 cgg gcc tcg tgc aag tca tgc cgg tcc cct atc gcc aag gac cag ctc 96
 45 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
 46 20 25 30
 48 cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144
 49 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
 50 35 40 45
 52 atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aaa 192
 53 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
 54 50 55 60
 56 tcc gtt gac gat gtt gaa ggg ata gat gca ctt aga tgg gat gat caa 240
 57 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
 58 65 70 75 80
 60 gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct 288
 61 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
 62 85 90 95
 64 aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc 336
 65 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
 66 100 105 110

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| 69 | Arg | Thr | Ser | Cys | Arg | Arg | Cys | Ser | Glu | Lys | Ile | Thr | Lys | Gly | Ser | Val | |
| 70 | | | 115 | | | | 120 | | | | | | 125 | | | | |
| 72 | cgt | ctt | tca | gct | aag | ctt | gag | agt | gaa | ggt | ccc | aag | ggt | ata | cca | tgg | 432 |
| 73 | Arg | Leu | Ser | Ala | Lys | Leu | Glu | Ser | Glu | Gly | Pro | Lys | Gly | Ile | Pro | Trp | |
| 74 | | | 130 | | | | 135 | | | | | | 140 | | | | |
| 76 | tat | cat | gcc | aac | tgt | ttc | ttt | gag | gta | tcc | ccg | tct | gca | act | gtt | gag | 480 |
| 77 | Tyr | His | Ala | Asn | Cys | Phe | Phe | Glu | Val | Ser | Pro | Ser | Ala | Thr | Val | Glu | |
| 78 | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| 80 | aag | ttc | tca | ggc | tgg | gat | act | ttg | tcc | gat | gag | gat | aag | aga | acc | atg | 528 |
| 81 | Lys | Phe | Ser | Gly | Trp | Asp | Thr | Leu | Ser | Asp | Glu | Asp | Lys | Arg | Thr | Met | |
| 82 | | | | 165 | | | | | | 170 | | | | | | 175 | |
| 84 | ctc | gat | ctt | gtt | aaa | aaa | gat | gtt | ggc | aac | aat | gaa | caa | aat | aag | ggt | 576 |
| 85 | Leu | Asp | Leu | Val | Lys | Lys | Asp | Val | Gly | Asn | Asn | Glu | Gln | Asn | Lys | Gly | |
| 86 | | | | 180 | | | | | | 185 | | | | | | 190 | |
| 88 | tcc | aag | cgc | aag | aaa | agt | gaa | aat | gat | att | gat | agc | tac | aaa | tcc | gcc | 624 |
| 89 | Ser | Lys | Arg | Lys | Lys | Ser | Glu | Asn | Asp | Ile | Asp | Ser | Tyr | Lys | Ser | Ala | |
| 90 | | | 195 | | | | | 200 | | | | | | | | 205 | |
| 92 | agg | tta | gat | gaa | agt | aca | tct | gaa | ggt | aca | gtg | cga | aac | aaa | ggg | caa | 672 |
| 93 | Arg | Leu | Asp | Glu | Ser | Thr | Ser | Glu | Gly | Thr | Val | Arg | Asn | Lys | Gly | Gln | |
| 94 | | | 210 | | | | | 215 | | | | | | | | 220 | |
| 96 | ctt | gta | gac | cca | cgt | ggt | tcc | aat | act | agt | tca | gct | gat | atc | caa | cta | 720 |
| 97 | Leu | Val | Asp | Pro | Arg | Gly | Ser | Asn | Thr | Ser | Ser | Ala | Asp | Ile | Gln | Leu | |
| 98 | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| 100 | aag | ctt | aag | gag | caa | agt | gac | aca | ctt | tgg | aag | tta | aag | gat | gga | ctt | 768 |
| 101 | Lys | Leu | Lys | Glu | Gln | Ser | Asp | Thr | Leu | Trp | Lys | Leu | Lys | Asp | Gly | Leu | |
| 102 | | | | 245 | | | | | | 250 | | | | | | 255 | |
| 104 | aag | act | cat | gta | tcg | gct | gct | gaa | tta | agg | gat | atg | ctt | gag | gct | aat | 816 |
| 105 | Lys | Thr | His | Val | Ser | Ala | Ala | Glu | Leu | Arg | Asp | Met | Leu | Glu | Ala | Asn | |
| 106 | | | | 260 | | | | | | 265 | | | | | | 270 | |
| 108 | ggg | cag | gat | aca | tca | gga | cca | gaa | agg | cac | cta | ttg | gat | cgc | tgt | gcg | 864 |
| 109 | Gly | Gln | Asp | Thr | Ser | Gly | Pro | Glu | Arg | His | Leu | Leu | Asp | Arg | Cys | Ala | |
| 110 | | | | 275 | | | | | | 280 | | | | | | 285 | |
| 112 | gat | gga | atg | cta | ttt | gga | gcg | ctg | ggt | cct | tgc | cca | gtc | tgt | gct | aat | 912 |
| 113 | Asp | Gly | Met | Leu | Phe | Gly | Ala | Leu | Gly | Pro | Cys | Pro | Val | Cys | Ala | Asn | |
| 114 | | | 290 | | | | 295 | | | | | | | | | 300 | |
| 116 | ggc | atg | tac | tat | tat | aat | ggt | cag | tac | caa | tgc | agt | ggt | aat | gtg | tca | 960 |
| 117 | Gly | Met | Tyr | Tyr | Tyr | Asn | Gly | Gln | Tyr | Gln | Cys | Ser | Gly | Asn | Val | Ser | |
| 118 | 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| 120 | gag | tgg | tcc | aag | tgt | aca | tac | tct | gcc | aca | gaa | cct | gtc | cgc | gtt | aag | 1008 |
| 121 | Glu | Trp | Ser | Lys | Cys | Thr | Tyr | Ser | Ala | Thr | Glu | Pro | Val | Arg | Val | Lys | |
| 122 | | | | 325 | | | | | | 330 | | | | | | 335 | |
| 124 | aag | aag | tgg | caa | att | cca | cat | gga | aca | aag | aat | gat | tac | ctt | atg | aag | 1056 |
| 125 | Lys | Lys | Trp | Gln | Ile | Pro | His | Gly | Thr | Lys | Asn | Asp | Tyr | Leu | Met | Lys | |
| 126 | | | | 340 | | | | | | 345 | | | | | | 350 | |
| 128 | tgg | ttc | aaa | tct | caa | aag | gtt | aag | aaa | cca | gag | agg | gtt | ctt | cca | cca | 1104 |
| 129 | Trp | Phe | Lys | Ser | Gln | Lys | Val | Lys | Lys | Pro | Glu | Arg | Val | Leu | Pro | Pro | |
| 130 | | | | 355 | | | | | | 360 | | | | | | 365 | |
| 132 | atg | tca | cct | gag | aaa | tct | gga | agt | aaa | gca | act | cag | aga | aca | tca | ttg | 1152 |

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| 133 | Met | Ser | Pro | Glu | Lys | Ser | Gly | Ser | Lys | Ala | Thr | Gln | Arg | Thr | Ser | Leu | |
| 134 | | 370 | | | | | 375 | | | | | 380 | | | | | |
| 136 | ctg | tct | tct | aaa | ggg | ttg | gat | aaa | tta | agg | ttt | tct | ggt | gta | gga | caa | 1200 |
| 137 | Leu | Ser | Ser | Lys | Gly | Leu | Asp | Lys | Leu | Arg | Phe | Ser | Val | Val | Gly | Gln | |
| 138 | 385 | | | | | | 390 | | | | 395 | | | | | 400 | |
| 140 | tca | aaa | gaa | gca | gca | aat | gag | tgg | att | gag | aag | ctc | aaa | ctt | gct | ggt | 1248 |
| 141 | Ser | Lys | Glu | Ala | Ala | Asn | Glu | Trp | Ile | Glu | Lys | Leu | Lys | Leu | Ala | Gly | |
| 142 | | | | | 405 | | | | | 410 | | | | | 415 | | |
| 144 | gcc | aac | ttc | tat | gcc | agg | gtt | gtc | aaa | gat | att | gat | tgt | tta | att | gca | 1296 |
| 145 | Ala | Asn | Phe | Tyr | Ala | Arg | Val | Val | Lys | Asp | Ile | Asp | Cys | Leu | Ile | Ala | |
| 146 | | | | 420 | | | | | 425 | | | | | 430 | | | |
| 148 | tgt | ggt | gag | ctc | gac | aat | gaa | aat | gct | gaa | gtc | agg | aaa | gca | agg | agg | 1344 |
| 149 | Cys | Gly | Glu | Leu | Asp | Asn | Glu | Asn | Ala | Glu | Val | Arg | Lys | Ala | Arg | Arg | |
| 150 | | | 435 | | | | | 440 | | | | | 445 | | | | |
| 152 | ctg | aag | ata | cca | att | gta | agg | gag | ggt | tac | att | gga | gaa | tgt | gtt | aaa | 1392 |
| 153 | Leu | Lys | Ile | Pro | Ile | Val | Arg | Glu | Gly | Tyr | Ile | Gly | Glu | Cys | Val | Lys | |
| 154 | 450 | | | | | | 455 | | | | | 460 | | | | | |
| 156 | aga | aca | aaa | tgc | tgc | cat | ttg | att | tgt | ata | aac | tgg | aat | gcc | tta | gag | 1440 |
| 157 | Arg | Thr | Lys | Cys | Cys | His | Leu | Ile | Cys | Ile | Asn | Trp | Asn | Ala | Leu | Glu | |
| 158 | 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| 160 | tcc | tca | aaa | ggc | mgt | act | gtc | act | gtt | aaa | ggt | aag | ggc | cga | agt | gct | 1488 |
| W--> 161 | Ser | Ser | Lys | Gly | Xaa | Thr | Val | Thr | Val | Lys | Val | Lys | Gly | Arg | Ser | Ala | |
| 162 | | | | 485 | | | | | | 490 | | | | | 495 | | |
| 164 | tgt | tca | tta | agt | cct | cyg | gtt | tgc | aag | aat | act | gct | cac | att | cct | tra | 1536 |
| W--> 165 | Cys | Ser | Xaa | Ser | Pro | Xaa | Val | Cys | Lys | Asn | Thr | Ala | His | Ile | Pro | Xaa | |
| 166 | | | | 500 | | | | | 505 | | | | | 510 | | | |
| W--> 168 | gra | tgg | gaa | aag | cat | ata | caa | tgc | amc | ctt | aaa | cat | gtt | ctg | acc | tgn | 1584 |
| W--> 169 | Xaa | Trp | Glu | Lys | His | Ile | Gln | Cys | Xaa | Leu | Lys | His | Val | Leu | Thr | Xaa | |
| 170 | | | 515 | | | | | 520 | | | | | 525 | | | | |
| W--> 172 | cac | nag | gtg | tgy | aca | ggc | tac | tat | gta | ctc | cag | atc | att | gaa | cag | gat | 1632 |
| W--> 173 | His | Xaa | Val | Cys | Thr | Gly | Tyr | Tyr | Val | Leu | Gln | Ile | Ile | Glu | Gln | Asp | |
| 174 | | 530 | | | | | 535 | | | | | 540 | | | | | |
| 176 | gat | ggg | tct | gag | tgc | tac | gta | ttt | cgt | aag | tgg | gga | cgg | gtt | ggg | agt | 1680 |
| 177 | Asp | Gly | Ser | Glu | Cys | Tyr | Val | Phe | Arg | Lys | Trp | Gly | Arg | Val | Gly | Ser | |
| 178 | 545 | | | | | 550 | | | | | 555 | | | | | 560 | |
| 180 | gag | aaa | att | gga | ggg | caa | aaa | ctg | gag | gag | atg | tca | aaa | act | gag | gca | 1728 |
| 181 | Glu | Lys | Ile | Gly | Gly | Gln | Lys | Leu | Glu | Glu | Met | Ser | Lys | Thr | Glu | Ala | |
| 182 | | | | 565 | | | | | 570 | | | | | 575 | | | |
| 184 | atc | aag | gaa | ttc | aaa | aga | tta | ttt | ctt | gag | aag | act | gga | aac | tca | tgg | 1776 |
| 185 | Ile | Lys | Glu | Phe | Lys | Arg | Leu | Phe | Leu | Glu | Lys | Thr | Gly | Asn | Ser | Trp | |
| 186 | | | 580 | | | | | 585 | | | | | 590 | | | | |
| 188 | gaa | gct | tgg | gaa | tgt | aaa | acc | aat | ttt | cgg | aag | cag | cct | ggg | aga | ttt | 1824 |
| 189 | Glu | Ala | Trp | Glu | Cys | Lys | Thr | Asn | Phe | Arg | Lys | Gln | Pro | Gly | Arg | Phe | |
| 190 | | | 595 | | | | | 600 | | | | | 605 | | | | |
| 192 | tac | cca | ctt | gat | gtt | gat | tat | ggt | gtt | aag | aaa | gca | cca | aaa | cgg | aaa | 1872 |
| 193 | Tyr | Pro | Leu | Asp | Val | Asp | Tyr | Gly | Val | Lys | Lys | Ala | Pro | Lys | Arg | Lys | |
| 194 | | 610 | | | | | 615 | | | | | 620 | | | | | |
| 196 | gat | atc | agt | gaa | atg | aaa | agt | tct | ctt | gct | cct | caa | ttg | cta | gaa | ctc | 1920 |
| 197 | Asp | Ile | Ser | Glu | Met | Lys | Ser | Ser | Leu | Ala | Pro | Gln | Leu | Leu | Glu | Leu | |

RAW SEQUENCE LISTING

DATE: 08/14/2001

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\08142001\I236995B.raw

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201 Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
202          645          650          655
W--> 204 ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra 2016
205 Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
206          660          665          670
W--> 208 aat att gag raa gga ttt gaa gca tta act krg rta cmg rat tta ttt 2064
209 Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
210          675          680          685
W--> 212 gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg 2112
W--> 213 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
214          690          695          700
W--> 216 ttg ytg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc 2160
217 Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
218 705          710          715          720
220 ata tta tac ggg atg agg atg att tca tat tca aag gcg aaa atg ctt 2208
221 Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
222          725          730          735
224 gaa gct ctg cag gat att gaa att gct tca aag ata gtt ggc ttc gat 2256
225 Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
226          740          745          750
228 agc gac agt gat gaa tct ctt gat gat aaa tat atg aaa ctt cac tgt 2304
229 Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
230          755          760          765
232 gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag 2352
233 Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
234          770          775          780
236 cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcg ctg 2400
237 Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
238 785          790          795          800
240 gaa ctg gag gaa gtt ttt tca ctt gat cga gat gga gaa ctt aat aag 2448
241 Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
242          805          810          815
244 tac tca aga tat aaa aat aat ctg cat aac aag atg cta tta tgg cac 2496
245 Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
246          820          825          830
248 ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga 2544
249 Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
250          835          840          845
252 att gca cct cct gag gca cct gtt act ggc tat atg ttc ggc aaa ggc 2592
253 Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
254          850          855          860
256 ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg 2640
257 Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val
258 865          870          875          880
260 gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta 2688
261 Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu
262          885          890          895

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265 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
266          900          905          910
268 aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag 2784
269 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
270          915          920          925
272 tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag 2832
273 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Pro Cys Gly Lys
274          930          935          940
276 ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac 2880
277 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
278 945          950          955          960
280 atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg 2928
281 Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val
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303 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
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305 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
306          35          40          45
307 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
308          50          55          60
309 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
310 65          70          75          80
311 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
312          85          90          95
313 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
314          100          105          110
315 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
316          115          120          125
317 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
318          130          135          140
319 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
320 145          150          155          160
321 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
322          165          170          175

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\08142001\I236995B.raw

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L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
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L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/236,995B

DATE: 08/14/2001

TIME: 15:53:57

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\08142001\I236995B.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Mahajan, Pramod B.
 4 Zuo, Zhuang
 6 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and Its Uses
 8 <130> FILE REFERENCE: 5718-34, 035718-174234
 10 <140> CURRENT APPLICATION NUMBER: 09/236,995B
 11 <141> CURRENT FILING DATE: 1999-01-26
 13 <150> PRIOR APPLICATION NUMBER: 60/072,785
 14 <151> PRIOR FILING DATE: 1998-01-27
 16 <160> NUMBER OF SEQ ID NOS: 5
 18 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

508 <210> SEQ ID NO: 5
 509 <211> LENGTH: 530
 510 <212> TYPE: DNA
 511 <213> ORGANISM: Zea mays
 513 <400> SEQUENCE: 5
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 516 caagaagaac cagataaaat ccgttgacga tgttgaagg atagatgcac ttagatggga 180
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 521 tgttgagaag ttctcaggct gggatacttt gtccgatgag gataagagaa ccatgctcga 480
 522 tcttggtaaa aaagatggtg gcaacaatga acaaaataag ggttccaagc 530

E--> 528 - 6 -

W--> 530 Alston & Bird

W--> 532 Alston & Bird

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/236,995B

DATE: 08/14/2001

TIME: 15:53:58

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\08142001\I236995B.raw

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L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
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L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:529 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:530 SEQ:5
L:530 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:532 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:532 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3